Fig. 6

Comparison of amino acid sequences "stripped-down" version of
chimera, known as "PigKS" (also called "Pig-Lys") vs. Pig uricase

<u>"Pig KS" uricase</u>:
Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

<u>Pig uricase</u>:
Pig cDNA from 1 to 915 (end)

[GCG GAP program]
Gap Weight: 12   Average Match: 2.912
    Length Weight: 4   Average Mismatch: -2.003

              Quality: 1601   Length: 319
                Ratio: 5.249   Gaps: 0
    Percent Similarity: 99.672   Percent Identity: 99.344

          Match display thresholds for the alignment(s):
                        | = IDENTITY
                        : = 2
                        . = 1

    pigKS.pep x Pig.pep   June 25, 1998 17:11 ..

pigKS 1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Pig   1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50

      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100

     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP 150
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP 150

     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200

     201 QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTLGQV 250
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     201 QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTLGQV 250

     251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL 300
         |||||||||||||||||||||||||||||||||||||||||:|||||||||
     251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGRITGTVKRKL 300

     301 SSRL* 305
         .||||
     301 TSRL*. 305

Fig. 7

Comparison of amino acid sequences of the "original" Pig-baboon
chimeric uricase ("chimera") with that of the "stripped-down" version
of chimera, known as "PigKS" (also called "Pig-Lys")

"Chimera" uricase:
Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to
915 (end)

"Pig KS" uricase:
Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

[GCG GAP program]
```
        Gap Weight:       12     Average Match:    2.912
     Length Weight:        4     Average Mismatch: -2.003

           Quality:    1589             Length:      319
             Ratio:   5.210               Gaps:        0
Percent Similarity:  98.689     Percent Identity:   98.689

        Match display thresholds for the alignment(s):
                          | = IDENTITY
                          : = 2
                          . = 1

chimera.pep x pigKS.pep    June 25, 1998 16:15   ..
```

```
chim.   1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
          |||||||||||||||||||||||||||||||||||||||||||||||||
PigKS   1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50

       51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100
          |||||||||||||||||||||||||||||||||||||||||||||||||
       51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100

      101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP 150
          |||||||||||||||||||||||||||||||||||||||||||||||||
      101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP 150

      151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
          |||||||||||||||||||||||||||||||||||||||||||||||||
      151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200

      201 QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
          ||||||||||||||||||||||||||||||||||||||||||.|  .|
      201 QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTLGQV 250

      251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL 300
          ||||||||||||||| |||||||||||||||||||||||||||||||||
      251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL 300

      301 SSRL*. 305
          |||||
      301 SSRL* 305
```

Fig. 8

Comparison of amino acid sequences of the "original" Pig-baboon
chimeric uricase ("chimera") with that of Pig uricase

"Chimera" uricase:
Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to
915 (end)

Pig uricase:
Pig cDNA from 1 to 915 (end)

[GCG GAP program]
Gap Weight: 12   Average Match: 2.912
     Length Weight: 4   Average Mismatch: -2.003

              Quality: 1583   Length: 305
               Ratio: 5.190   Gaps: 0
Percent Similarity: 98.361   Percent Identity: 98.033

       Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =   2
                   . =   1

chimera.pep x Pig.pep   June 25, 1998 16:54   ..


```
chim   1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Pig    1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50

      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100

     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP 150

     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200

     201 QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
         ||||||||||||||||||||||||||||||||||||||||||||||.|.| 
     201 QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTLGQV 250

     251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL 300
         |||||||||||||||||| |||||||||||||||||||||||:||||||| 
     251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGRITGTVKRKL 300

     301 SSRL* 305
         .||||
     301 TSRL* 305
```